

Please replace the paragraph beginning at page 8, line 12, with the following rewritten paragraph:

--FIG. 14A-B. Predominant expression of STEAP-2 (98P4B6) in prostate tissue. First strand cDNA was prepared from 8 normal tissues, the LAPC xenografts (4AD, 4A1 and 9AD) and HeLa cells. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 98P4B6, shows predominant expression of 98P4B6 in normal prostate and the LAPC xenografts. The following primers were used to amplify STEAP II:

98P4B6.1 5'GACTGAGCTGGAAGTGAATTTGT 3' (SEQ ID NO:17)

98P4B6.2 5' TTTGAGGAGACTTCATCTCACTGG 3' (SEQ ID NO:18)--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'atatgccgcgctcgtcgtcgacaa3' (SEQ ID NO:30) and 5'agccacacgcagctcattgtagaagg 3' (SEQ ID NO:31) to amplify β -actin. First strand cDNA (5 μ l) was amplified in a total volume of 50 μ l containing 0.4 μ M primers, 0.2 μ M each dNTPs, 1XPCR buffer (Clontech, 10mM Tris-HCL, 1.5 mM MgCl₂, 50 mM KCL, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five μ l of the PCR reaction was removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycle under the following conditions: initial denaturation was at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 bp β -actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β -actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization were required to achieve equal band intensities in all tissues after 22 cycles of PCR--

Please replace the paragraph beginning at page 42, line 10, with the following rewritten paragraph:

--Example 3D: Immunohistochemical Analysis of STEAP-1 Protein Expression in Prostate Tumor Biopsy and Surgical Specimens

To determine the extent of STEAP-1 protein expression in clinical materials, tissue sections were prepared from a variety of prostate cancer biopsies and surgical samples for immunohistochemical analysis. Tissues were fixed in 10% formalin, embedded in paraffin, and sectioned according to standard protocol. Formalin-fixed, paraffin-embedded sections of LNCaP cells were used as a positive control. Sections were stained with an anti-STEAP-1 polyclonal antibody directed against a STEAP-1 N-terminal epitope (as described immediately above). LNCaP sections were stained in the presence of an excess amount of the STEAP-1 N-terminal peptide immunogen used to generate the polyclonal antibody (peptide 1) or a non-specific peptide derived from a distinct region of the STEAP-1 protein (peptide 2; YQQVQQNKEDAWIEH). (SEQ ID NO:32)--